

FIG. 1

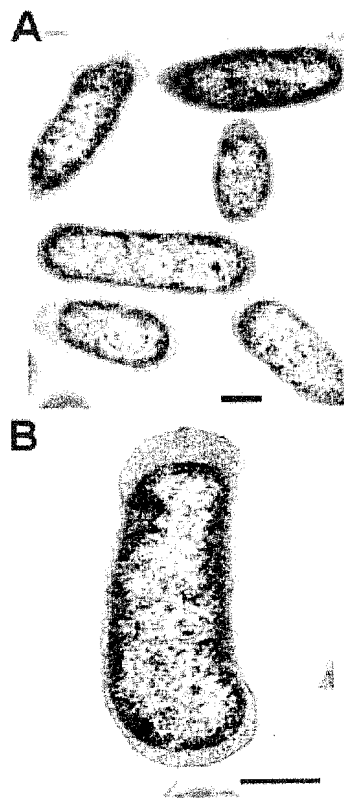


FIG. 2

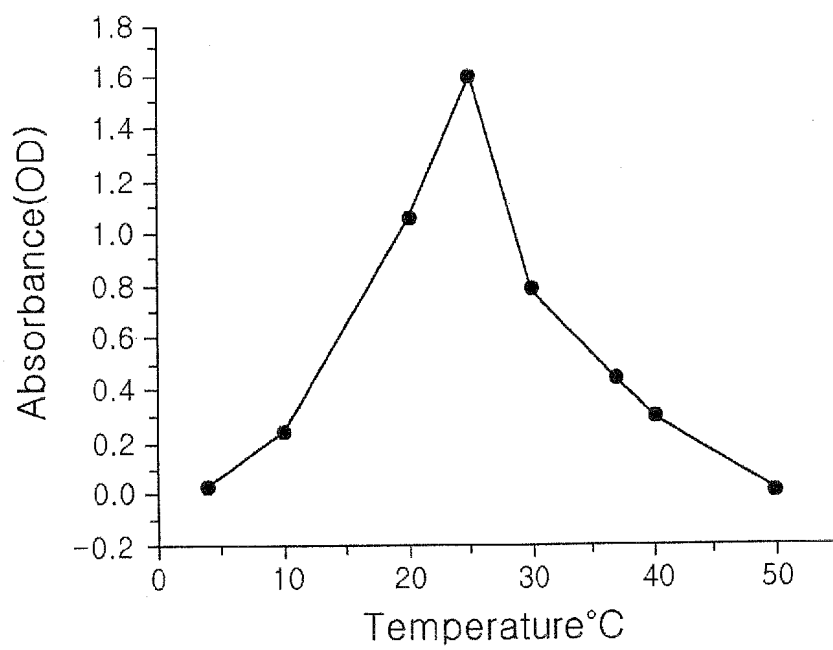


FIG. 3

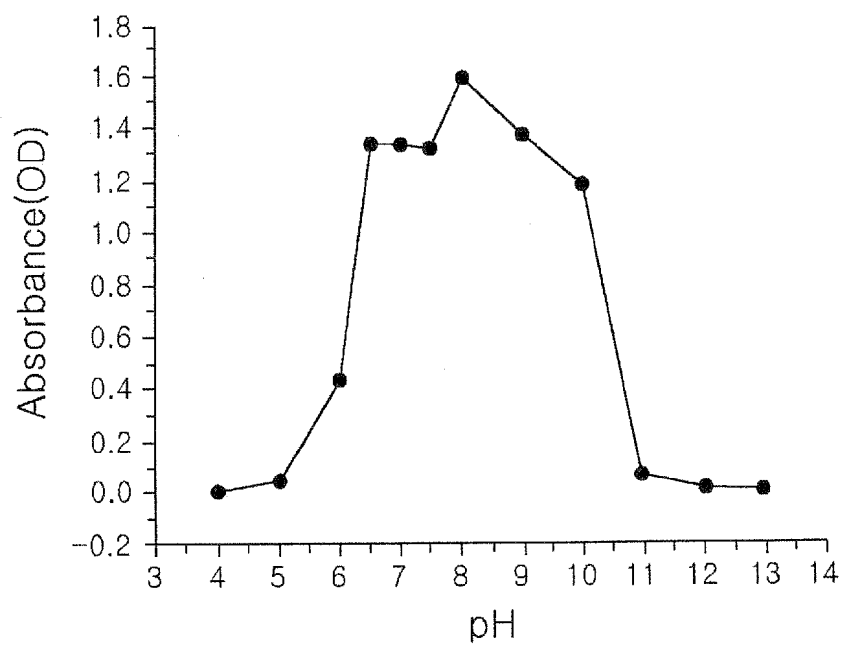


FIG. 4

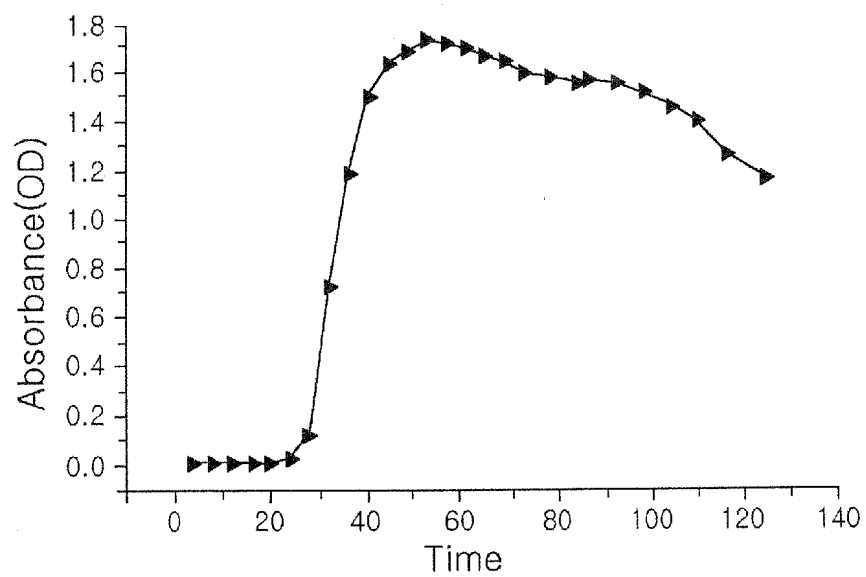


FIG. 5

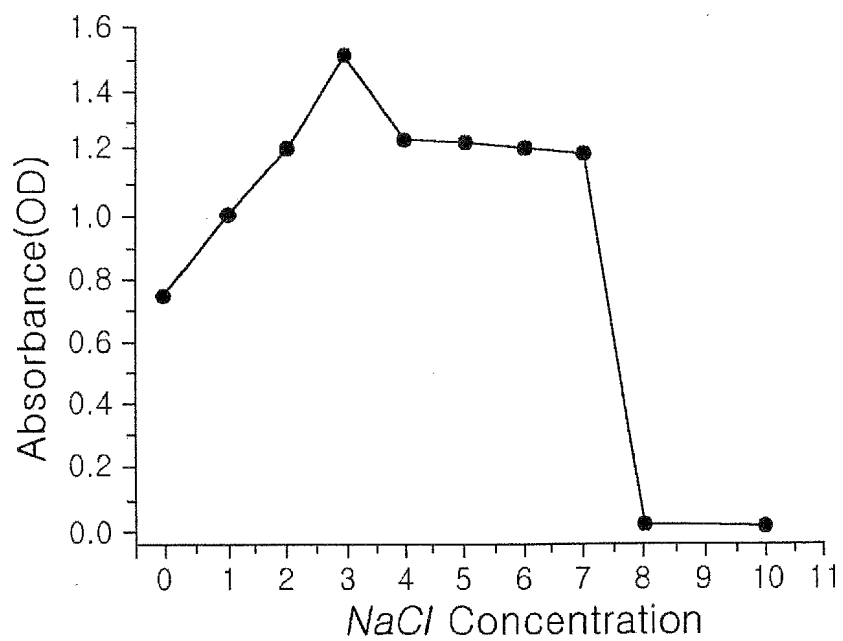


FIG. 6

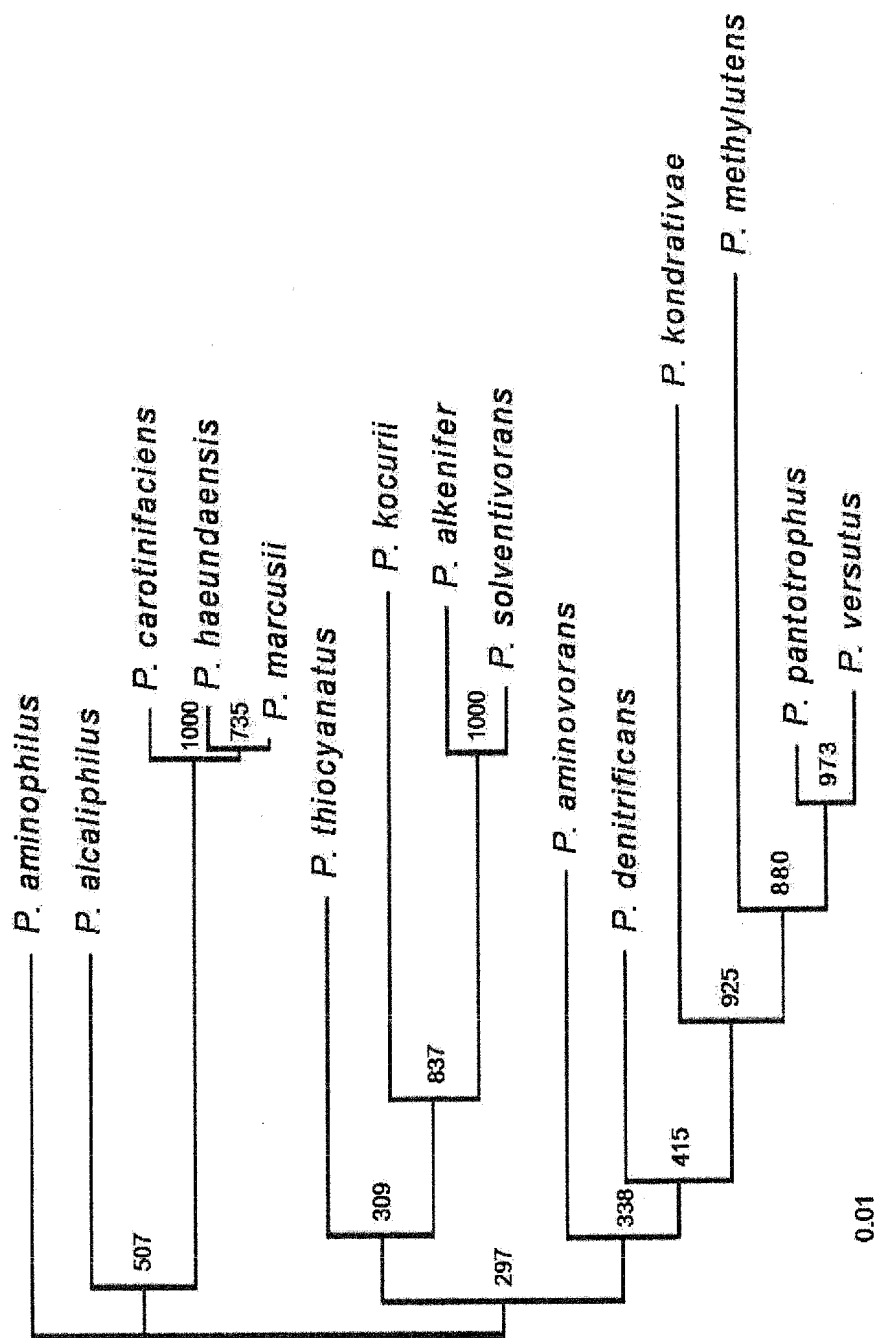


FIG. 7

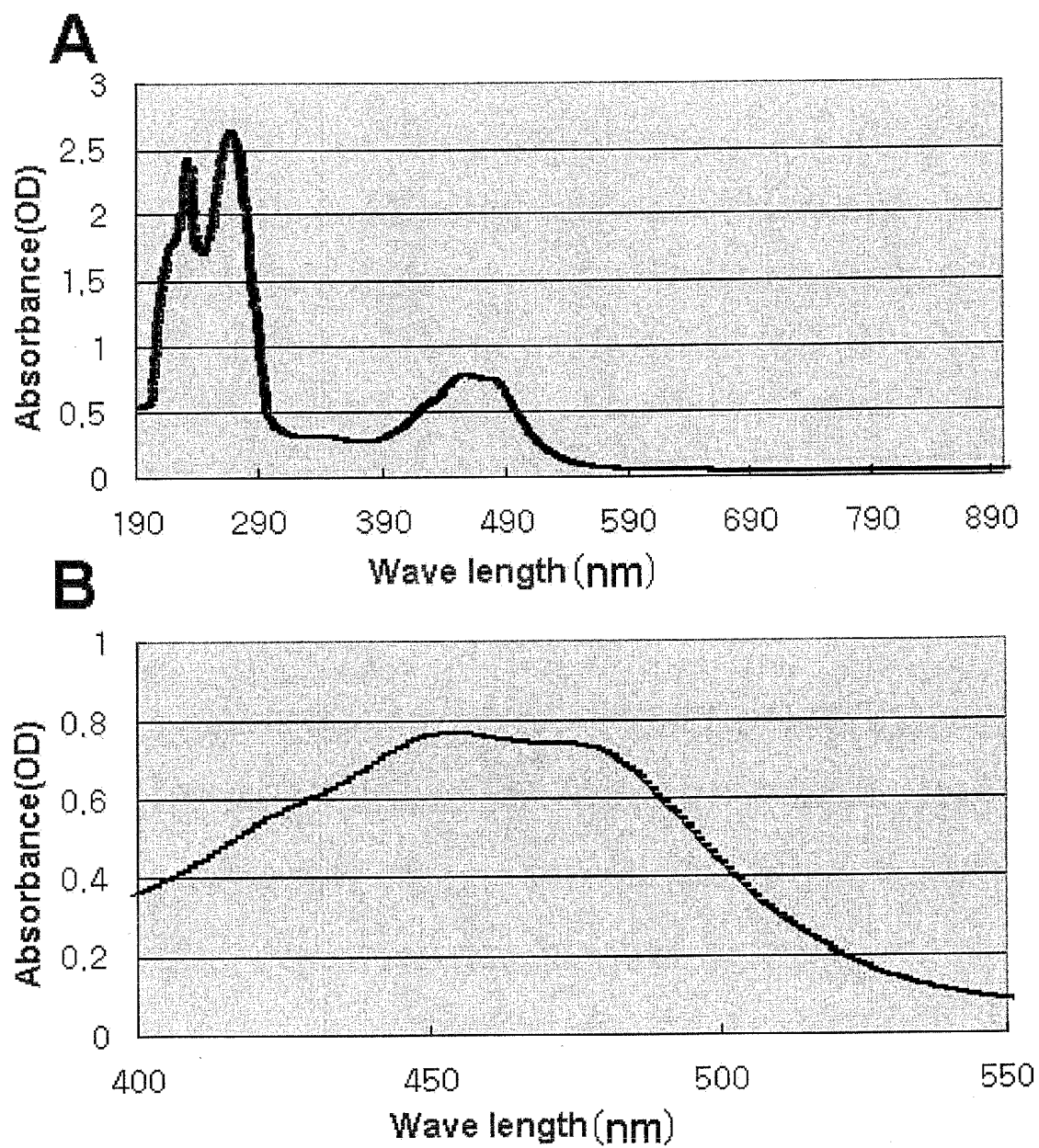


FIG. 8

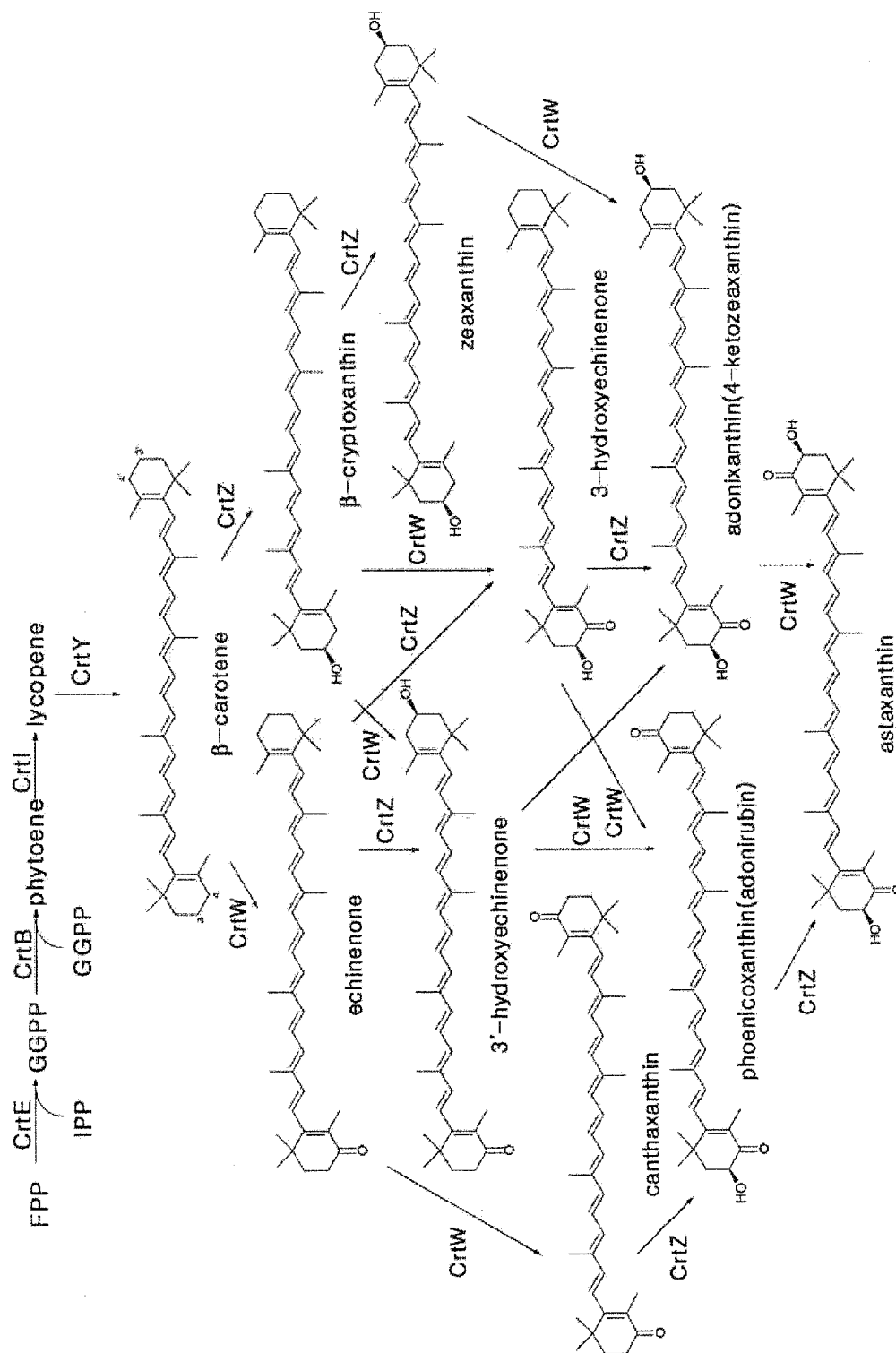


FIG. 9

| | | |
|---------------------------|-------|--|
| | 1 | 100 |
| <i>P. haemdaesis</i> | (1) | -----NSAHALPKADLTATSLVSGGLTAADLALHVAHWFLDAARHPILATIANFGLT-WLSVGLFTIADAHNGSVYPGPRKGNANAGQLVLD |
| <i>Alcaligenes</i> _sp | (1) | -----NSGRKPGTTGDTIVNGLTAAILLICVLYLRAETLWLLDAARHPLLAVELCLAGLT-WLSVGLFTIADAHNGSVYPGPRANAAAGQLALW |
| <i>Bradyrhizobium</i> _sp | (1) | NHAATAKATEFGASRRDDARQRVGLTAAVTIAATLYLVGLNFFWPLTLLSLPALPLVVLQTLVYGLFTIADCHNGSLVPEHPQYWRRIQGLCLF |
| Consensus | (1) | MSAKATVLSAALTAANLYLHV LWFDAARHPLLAAILLGLT WLSVGLFTIADAHNGSVYPGPRANAAAGQL LW |
| | 101 | 200 |
| <i>P. haemdaesis</i> | (90) | LYAGESWRNVIYKHNHHHRTGDDDDPDEHG---GPVRVAREFTGTFGWRGELLIPVITVYAILGD-RWNYVFWPLPSILASIQLEVEGTWLPHR |
| <i>Alcaligenes</i> _sp | (90) | LYAGESWPKLIANKHTHHRAGTDNDEFGHG---GPVWVGSFSTYFGWRGELLIPVITVYAILGD-RWNYVFWPVAVASIQTFVEGTWLPHR |
| <i>Bradyrhizobium</i> _sp | (101) | LYAGESFDALNVEHKKHHRHPTAEDPDEVPFGHNWTFASFLHVEGKQVALIAVSLVYQLVFAPPLQNLLEWALPGLLSALQLEFEGTYLPHK |
| Consensus | (101) | LYAGESW KLIYKHN HHRH GTDDDDPDEHG GPVWVASFITYEGWRGELLIPVITVYAILGD RWNYVFWPLPAILASIQLEVEGTWLPHR |
| | 201 | 259 |
| <i>P. haemdaesis</i> | (186) | PGHDAEPDRHNAESSRISDPVSLTCTFEGGYHHEHLEHPTVPWRLPSTRTKGDI A-- |
| <i>Alcaligenes</i> _sp | (186) | PGHDEPDRHNAESTGIDPLSLTCTFEGGYHHEHLEHPTVPWRLPSTRTKGDA-- |
| <i>Bradyrhizobium</i> _sp | (201) | PAIQPADRHNAITSEPPANLSLTCTFEG-FHHEHLEHPTAPWRLDEIKRRLERD |
| Consensus | (201) | PGHD PDRHNAESS I DPLSLTCTFEGGYHHEHLEHPTVPWRLP TRKGA A |

FIG. 10

| | | |
|----------------------|--|-----|
| | 1 | 100 |
| P. haemdaesis (1) | MTNELLIVVAIVLVNELTATSVSRNINHGSLGCGNKHSHHEEDHAEKNDLYGCVFATATVFTVGNTHAPVFWIATAGNTVGLTYFTLHDSLYREQW | |
| Alcaligenes_sp (1) | MTQFLIVVAIVLVNELTATSVSRNINHGSLGCGNKHSHHEEDHAEKNDLYGCVFATATLFTVGNTHAPVFWIATAGNTVGLTYFTLHDSLYREQW | |
| Consensus | (1) MTNELLIVVAIVLVNELTATSVSRNINHGSLGCGNKHSHHEEDHAEKNDLYGCVFATATLFTVGNTHAPVFWIATAGNTVGLTYFTLHDSLYREQW | |
| | 101 | 153 |
| P. haemdaesis (101) | PERVTPRNGTARRLYQAHLHHAVEGRDHCVSFGFIYAPPVVKLQDLKTSGVLRAEQERT | |
| Alcaligenes_sp (101) | PERVTPRNGTARRLYQAHLHHAVEGRDHCVSFGFIYAPPVVKLQDLKTSGVLRQDERPS | |
| Consensus | (101) PERVTPRNGY RRLYQAHLHHAVEGRDHCVSFGFIYAPPVVKLQDLK SGVLR S | |

FIG. 11

| | | | |
|-------------------|-------|--|-----|
| | 1 | | 100 |
| P. haemdaesis | (1) | VTHDVLLAGAGL ANGELIALALRAABPMLRVLLDHAAGES DGH TWS CHPDLSI SWLAEPLERAWPQCEVFPEHARRLAT GTGSLDGAALADAVAR | |
| Flavobacterium_sp | (1) | NSHDLLIAGAGLSGHLIALAYDRERDAKI VMLDARSSES DQHT WSCHT DLSPEWLARLSPIEGEWTDQCEVAFYDHSERLTT GTGSLAGALIGLLQ- | |
| Consensus | (1) | NSHDLLIAGAGLIA ALIALALR RPD KILLED AGESD HWSCHD DLSP WLARL PIRRA W DOEY FP HARRL TGVGSDAAAL L | |
| | 101 | | 200 |
| P. haemdaesis | (101) | SGAEIWNSDIALDEQALISOSTRIEAGAVLDGEGAPSRRLTVGEQKFGVVEITDCPHGVPREHINDATVTCQDGTRETYLLFPFSPTRILLIEDTRY | |
| Flavobacterium_sp | (100) | -GVDLEWTHVATLDDTGATLTDGSRTEAACVIDARGAVETPLTVGEQKFGVVEITDAPHGVERPHINDATVPQMDGTRETYLLFPFSPTRILLIEDTRY | |
| Consensus | (101) | G DIRWS IA LDD GATLS GSRIEAA VIDARGA S HLTGFGKFGVVEITD PHGV RPHINDATV Q DGTRETYLLFPFSPTRILLIEDTRY | |
| | 201 | | 300 |
| P. haemdaesis | (201) | SDGSLDLDALAAASHDYARQQWGTGAIVBEREGILLPI ALAHDAAGTADHREGPPVGLRAGFHPTGSLPYAAQVADVVAGLSGPPGTDALEGALR | |
| Flavobacterium_sp | (199) | SDGSLDDGALAQASLDYARRGWGTQENBEREGILLPI ALAHDAIGFWRDHAQAVPYGLGAGLEHPTGSLPYAAQVADALAR--DGTIASARAVE | |
| Consensus | (201) | SDGSL LDD ALA AS DYA GTTG ENBEREGILLPIALAHDA GEV DHA G VPVGL AG PHPTGSLPYAQVAD IAA T A R ALR | |
| | 301 | | 387 |
| P. haemdaesis | (301) | DYALDEARRDRFLELLNRMLFEGCAPDERFTLLOEFYRNMHGLIERFTAGRLSVANQLRI VTGKPTPLGTAIRCLPERILLKENA | |
| Flavobacterium_sp | (297) | GWALDEADRDRELELLNRMLFEGCPDREYMLLOEFYELFQPLIERFTAGRLTLADELRI VTGRPIPLSQAVCLPERILLQERA | |
| Consensus | (301) | WALDRA RDRFLELLNRMLEGC PDREY LLQREYRLP LIERFYAGRLSLAD LRIYGNPPIPL AIRCLPERILL E A | |

FIG. 12

| | | |
|-------------------|-------|--|
| | 1 | 100 |
| P. haeundaesis | (1) | MNAHSPA AKT XI VI GRGFGGLALAI RLQSAGI ATTLVEARDKPGGRAYVWHDQGHVEDAGPTVI TDDALKE LWA L TGQDNARDVT LMPVSPFFYELNWP G |
| Flavobacterium_sp | (1) | -----HSSAI VI GRGFGGLALAI RLQSAGI ATTI VEARDKPGGRAYVWHDQGHVEDAGPTVYTDPSLRELWALSGQPHREDVTLLPVSPFFYELTWAD |
| Consensus | (1) | S I VIGAGFGGLALAI RLQSAGI ATTI VEARDKPGGRAYVW DQGHVEDAGPTVI TDDALKE LWA LSGQ M EDVTLLPVSPFFYEL W |
| | 101 | 200 |
| P. haeundaesis | (101) | GKVEDYVNEADQLE RQIAQNEFDLEGYRRFRDYAEVYVQEGYVKLGT YFELKLGQMLKAAPALMKLEAYKSVHAKVATFIKDPYLBQAFSYHTLLVGN |
| Flavobacterium_sp | (94) | GRSEFYVNDDELL BQVASFNPADVDGYRRFHDYAEVYVREGYVKLGTTFELKLGQMLNAPALMRLLQAYESVHSGVAREFIQDPHLRQAFSEHTLLVGN |
| Consensus | (101) | GK FDYVND D L RQIA FNP DLDGYRRF DYAEVY EGYVKLGT FELKLGQML AAPALMKL AYKSVHA YA FI DPHLRQAFSEHTLLVGN |
| | 201 | 300 |
| P. haeundaesis | (201) | PFSTSSIYALIHALERGGVWF AKGGTNQLVAGNVALFERLGGQNM LNAKVARIETEGARTTGVT LADGRSLEADWVASNGDVHENVYEDLLIGHTAAGQSR |
| Flavobacterium_sp | (194) | PFSTSSIYALIHALERGGVWF AKGGTNQLVAGNVALFERLGGT LLNARVTRIDTEGDEATGVTLLDGRQL EADTVASNGDVHHSYEDLLIGHTBGGRTK |
| Consensus | (201) | PFSTSSIYALIHALERGGVWF AKGGTNQLVAGNVALFERLGG LLNAKV RIDTEG R TGVTL DGR LRAD VASNGDVNH YRDLIGHT RG SK |
| | 301 | 400 |
| P. haeundaesis | (301) | AKSLDKRWS LFLVHFGLE RPAKDIAHRTILFGPRYREL VNEIFKGPKLAEDES LYLHSPCTTDDMAPPGMSTHYVLAPVPHLGR AEIDWAVEGPERY |
| Flavobacterium_sp | (294) | AAILNQRWS LFLVHFGLSKRPENLAHSGVIEGPRYKGLVNEIFNRPRLPDDSNYLESPCVTDSLAPGCMSTHYVLAPVPHLGRADVDWEAREPGY |
| Consensus | (301) | A L R RWS LFLVHFG L P IAHRSIIFGPRYK LYNEIF GPKL DDFS LYLHSPC TDP LAP GCMSTHYVLAPVPHLGRADIDW EAP Y |
| | 401 | 500 |
| P. haeundaesis | (401) | ADRI LASLEERLIPNLKAMLTTRITPDAFASELNAHGSASFVEPILTQS AWEPHNEKDKT IENFYIVGACTHPGAGIPGVVGS AKAT AQQWLSDL AG |
| Flavobacterium_sp | (394) | AERIPEELERBAIPDLRKHLYTSEIFSPADSTELS AHGGSASFVEPILTQS AWEPHNEKDRAIPNFYIVGACTHPGAGIPGVVGS AKAT AQQWLSDLAV |
| Consensus | (401) | ADRI LE R IP LR LT SRI FSPADFASEL AHGGSASFVEPILTQS AWEPHNEKD K I NFYIVGACTHPGAGIPGVVGS AKAT AQQWLSDLA |
| | 501 | |
| P. haeundaesis | (501) | A |

FIG. 13

| | | |
|-------------------|---|-----|
| | 1 | 100 |
| P. haemdaesis | (1) MSDELTSTBAITQSGSQSF AAKLNEPQIRDDTYMLYANGCHADDVIDQALSSREAVNDPQALDGLRVDLAAIQSGPYTPPEAALRAVAREHDF | |
| Flavobacterium_sp | (1) NTDLTATSEAAIAQSGSQFQAQAKLPPGEIEDTYMYTANCERHADDVIDQVMSGAPFAGGDPQASLGALRADTLAALHEUGENSPFFAALLQVAREHDF | |
| Consensus | (1) MSDE TS AI QGSGSFA AAKLPPGEIRDDTYMYTANCERHADDVIDSQ IGS PEA DPQARL ALB DTLAAL DGPNSPFFAALR YAREHDF | |
| | 101 | 200 |
| P. haemdaesis | (101) PQAMPNDLIEGFANDVEARDYETLDVLEYSYHYAGTGVMMARVNGVRDPVLDRACDLGLAFQLTNIARDYIDDARIQECYLPGLDQAGARIDGPV | |
| Flavobacterium_sp | (101) PDLNPNDLIEGFANDVADREYESLDVLEYSYHYAGTGVMMARVNGVQDDAVLDRACDLGLAFQLTNIARDYIDDARIQECYLPADWLAEAGATVESEPV | |
| Consensus | (101) P WPNDLIEGFANDY HDYESLDVLEYSYHYAGTGVMMARVNGV DD VLDRACDLGLAFQLTNIARDYIDDA IGSCYLPADWL AGA IDGPV | |
| | 201 | 300 |
| P. haemdaesis | (201) PSPELYTVILELLEDAEPYVASRVGLADLPDRCANSTAAALRIYBALGEIENSGQAYRQDEISTSTAANKLGLGVGGVDVARSRLPGAGVSRQGLNTR | |
| Flavobacterium_sp | (201) PSDALYSVITRELLDAEPYVASRQGLPHLPDRCANSTAAALRIYBALGETRIQGGPEAYRQDEISTSTAANKLGLLAKGELDAHASRLGGETSEDEGLNTR | |
| Consensus | (201) PS LYSVITRELD AEPYVASR GL LPPRCANSTAAALRIYRANG RIR GP AYRQRLSTAAANKGLLA GG D A SRL GA ISE GLNTR | |
| | 301 | |
| P. haemdaesis | (301) PHHV | |
| Flavobacterium_sp | (301) PRA- | |
| Consensus | (301) P | |

FIG. 14

| | | |
|-------------------|-------|---|
| | 1 | 100 |
| P. haemdaesis | (1) | HERDYPITAIILQIREHIAQFEAVSQIDANSHGILSSGRERCHNILLAAEAGGVCTIIVDAQAVENVAHSLIFEDDLPCHDAQAKRGPAT |
| Flavobacterium_sp | (1) | WPKQPPIDRIVEIRIAQISQFGVYSIRLGAAKIDALSPGEPFVILNIVHSSGVGVCAWFOACAVENVAHSLIFEDNCHUDARTKGPAT |
| Consensus | (1) | N N LL BL IA EG VS PIGAAHS AHS GEFRAHMLL AEGSGVCD IVDACAVENVAHSLIFDDLPCHDDA RRG PAT |
| | 101 | 200 |
| P. haemdaesis | (101) | HVAHGESAVLGGTALITTEAHALLAGAKSGTVPAQVRIILSLGPQGLAGGQDILLHANGHGVREQDNTGVLEPTAGLENLAVIKETPAEQTQ |
| Flavobacterium_sp | (101) | HVAHGECAVLAGTALITTEAMRILGEARGTDPQAPLVAHSHRANGFVGLAGGQDILHAPDAAETERHODNTGVIFVAGLEHMSILKGLDKAETEQ |
| Consensus | (101) | HVAHGE BAVLAGLALITTEAN ILLA ARGAS RA LV LSRALGP GICGAGQDILHA X HAGLE EQDNTGVLEPTAGLENLAIK D E Q |
| | 201 | 295 |
| P. haemdaesis | (201) | MTDFGRQLGEVFQSYDLDLVNQDAALGKUTGRDAAPPRGELLAYSQIQVSHVTEAGACQIDAHESKNIQAPETALLENVDPYABA-- |
| Flavobacterium_sp | (201) | LMAGGRQLGEVFQSYDLDLVNEDVASTGKUTARITAAPGPKGLNAVQGVDAQHYEASACQIDELNETLEFGGQIADLLANVPHHRESA |
| Consensus | (201) | LI FGRQLGEVFQSYDLDLVYCD AA GKUTARD AAPPKV GLLAY L VA HY ASRAQID LRESK A IA LL RVLPB B |

FIG. 15

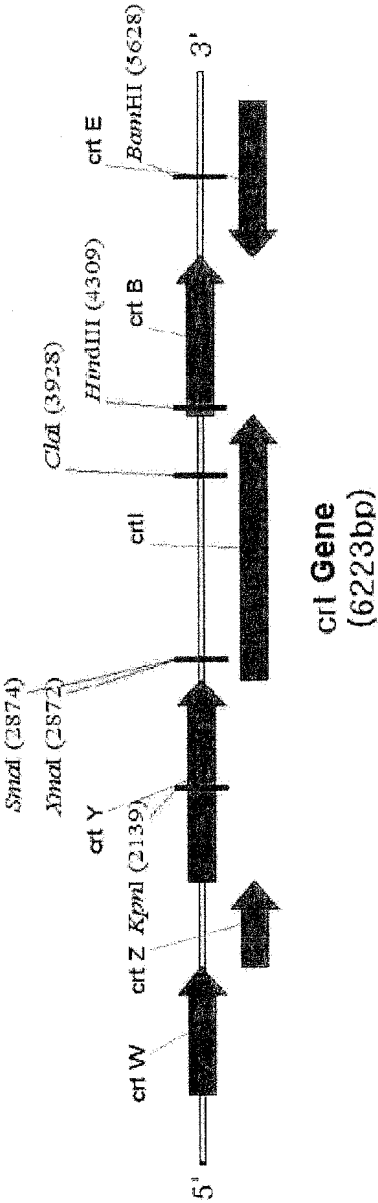


FIG. 16

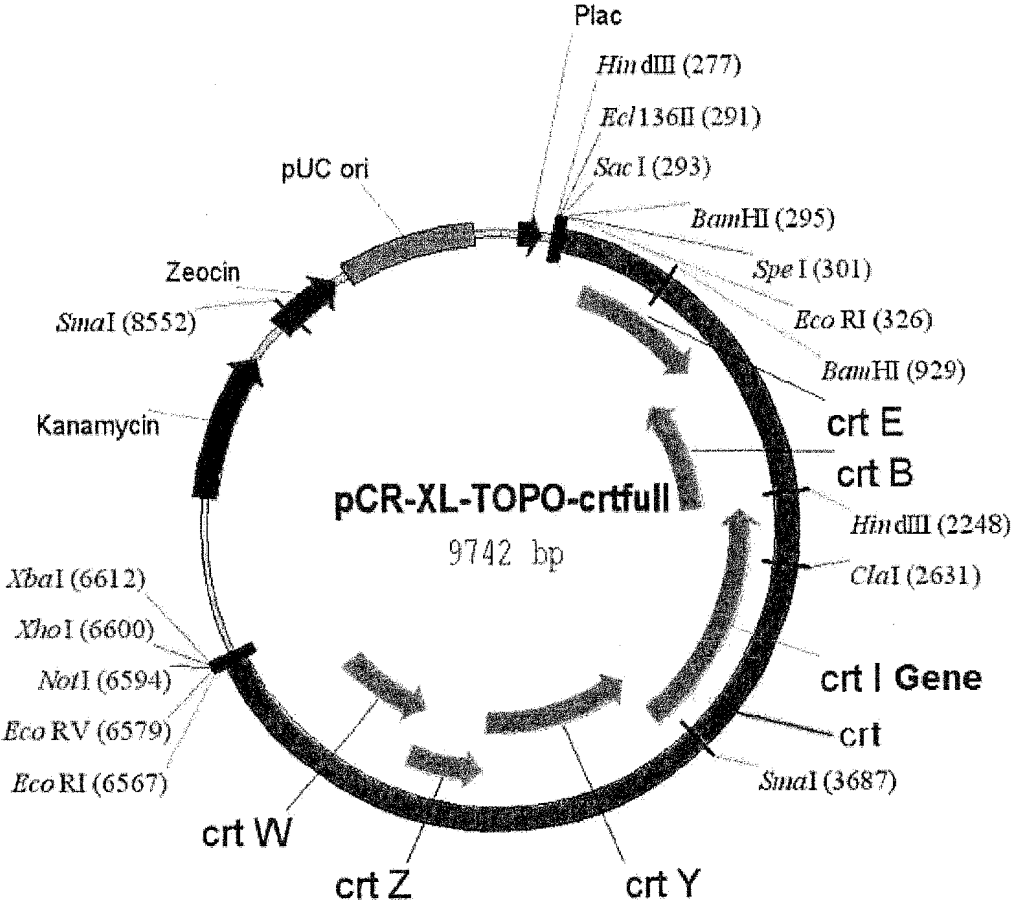


FIG. 17

